

SEQUENCE LISTING

<110> Saba, Julie D.

<120> COMPOSITIONS AND METHODS FOR THE MODULATION
OF SPHINGOLIPID METABOLISM AND/OR SIGNALING

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<141> 2003-07-16

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ccg gtg agg tta gca gtg aga aca tac gag cat agt tcc aga aga ttg	288
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Glu Val Thr Lys Val Lys Gln Ser Ile Glu Asp Glu Leu Ile Arg Ser	
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gac tct cag tta atg aat ttc cca cag ttg cca tcc aat ggg ata cct	432
Asp Ser Gln Leu Met Asn Phe Pro Gln Leu Pro Ser Asn Gly Ile Pro	
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Leu Ala Cys Leu Ser Ala Lys Met Tyr Ala Leu His His Arg Gly Ile	
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Lys Thr Ala Gly Val Ala Asp Lys Leu Ile Val Gly Phe Leu Asp Ala
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Lys Asp Glu Leu Glu Lys Ser Leu Arg Ile Val Asp Arg Ser Thr Glu	
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Val Gly Ser Ala Pro Asn Phe Pro Phe Gly Thr Val Asp Asp Ile Glu	
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Ala Ile Gly Gln Leu Gly Leu Glu Tyr Asp Ile Pro Val His Val Asp	
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Val	Lys	Ser	His	Lys	Pro	Ser	Glu	Ser	Asp	Lys	Thr	Ser	Glu	Ala	Ala
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 Ser Leu Trp Ser Arg Phe Lys Lys Lys Leu Phe Lys Leu Ile Arg Lys
 65 70 75 80
 atg cca ttt att gga cgt aag atc gaa caa cag gtg agc aaa gcc aag 288
 Met Pro Phe Ile Gly Arg Lys Ile Glu Gln Gln Val Ser Lys Ala Lys
 85 90 95
 aag gat ctt gtc aag aac atg cca ttc cta aag gtg gac aag gat tat 336
 Lys Asp Leu Val Lys Asn Met Pro Phe Leu Lys Val Asp Lys Asp Tyr
 100 105 110
 gtg aaa act ctg cct gct cag ggt atg ggc aca gct gag gtt ctg gag 384
 Val Lys Thr Leu Pro Ala Gln Gly Met Gly Thr Ala Glu Val Leu Glu
 115 120 125
 aga ctc aag gag tac agc tcc atg gat ggt tcc tgg caa gaa ggg aaa 432
 Arg Leu Lys Glu Tyr Ser Ser Met Asp Gly Ser Trp Gln Glu Gly Lys
 130 135 140
 gcc tca gga gct gtg tac aat ggg gaa ccg aag ctc acg gag ctg ctg 480
 Ala Ser Gly Ala Val Tyr Asn Gly Glu Pro Lys Leu Thr Glu Leu Leu
 145 150 155 160
 gtg cag gct tat gga gaa ttc acg tgg agc aat cca ctg cat cca gat 528
 Val Gln Ala Tyr Gly Glu Phe Thr Trp Ser Asn Pro Leu His Pro Asp
 165 170 175

atc ttc cct gga ttg cgg aag tta gag gca gaa atc gtt agg atg act	576
Ile Phe Pro Gly Leu Arg Lys Leu Glu Ala Glu Ile Val Arg Met Thr	
180 185 190	
tgt tcc ctc ttc aat ggg gga cca gat tcc tgt gga tgt gtg act tct	624
Cys Ser Leu Phe Asn Gly Gly Pro Asp Ser Cys Gly Cys Val Thr Ser	
195 200 205	
ggg gga acg gaa agc atc ctg atg gcc tgc aaa gct tac cgg gac ttg	672
Gly Gly Thr Glu Ser Ile Leu Met Ala Cys Lys Ala Tyr Arg Asp Leu	
210 215 220	
gcg tta gag aag ggg atc aaa act cca gaa att gtg gct ccc gag agt	720
Ala Leu Glu Lys Gly Ile Lys Thr Pro Glu Ile Val Ala Pro Glu Ser	
225 230 235 240	
gcc cat gct gca ttc gac aaa gca gct cat tat ttt ggg atg aag att	768
Ala His Ala Ala Phe Asp Lys Ala Ala His Tyr Phe Gly Met Lys Ile	
245 250 255	
gtc cga gtt gca ctg aaa aag aac atg gag gtg gat gtg cag gca atg	816
Val Arg Val Ala Leu Lys Lys Asn Met Glu Val Asp Val Gln Ala Met	
260 265 270	
aag aga gcc atc tcc agg aac aca gct atg ctg gtc tgt tct acc cca	864
Lys Arg Ala Ile Ser Arg Asn Thr Ala Met Leu Val Cys Ser Thr Pro	
275 280 285	
cag ttt cct cat ggt gtg atg gat cct gtc ccc gaa gtg gcc aag tta	912
Gln Phe Pro His Gly Val Met Asp Pro Val Pro Glu Val Ala Lys Leu	
290 295 300	
act gtc aga tat aaa atc cca ctc cat gtg gat gct tgt ctg ggg ggc	960
Thr Val Arg Tyr Lys Ile Pro Leu His Val Asp Ala Cys Leu Gly Gly	
305 310 315 320	
ttc ctc att gtc ttc atg gag aaa gca ggg tac cca ctg gag aaa cca	1008
Phe Leu Ile Val Phe Met Glu Lys Ala Gly Tyr Pro Leu Glu Lys Pro	
325 330 335	
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Phe Asp Phe Arg Val Lys Gly Val Thr Ser Ile Ser Ala Asp Thr His	
340 345 350	
aag tat ggc tat gct cct aaa ggt tca tca gtg gtg atg tac tct aac	1104
Lys Tyr Gly Tyr Ala Pro Lys Gly Ser Ser Val Val Met Tyr Ser Asn	
355 360 365	
gag aag tac agg acg tac cag ttc ttt gtt ggt gca gac tgg caa ggt	1152
Glu Lys Tyr Arg Thr Tyr Gln Phe Phe Val Gly Ala Asp Trp Gln Gly	
370 375 380	
ggt gtc tac gca tct cca agc ata gct ggc tca cgg cct ggt ggc atc	1200
Gly Val Tyr Ala Ser Pro Ser Ile Ala Gly Ser Arg Pro Gly Gly Ile	

385	390	395	400	
att gca gcc tgt tgg gcg gcc ttg atg cac ttc ggt gag aac ggc tat				1248
Ile Ala Ala Cys Trp Ala Ala Leu Met His Phe Gly Glu Asn Gly Tyr	405	410	415	
gtt gaa gct acc aaa cag atc atc aaa act gct cgc ttc ctg aag tca				1296
Val Glu Ala Thr Lys Gln Ile Ile Lys Thr Ala Arg Phe Leu Lys Ser	420	425	430	
gaa ctg gaa aac atc aaa aac atc ttc att ttc ggt gat cct caa ttg				1344
Glu Leu Glu Asn Ile Lys Asn Ile Phe Ile Phe Gly Asp Pro Gln Leu	435	440	445	
tca gtt att gct ctg gga tcc aac gat ttt gac att tac cga cta tct				1392
Ser Val Ile Ala Leu Gly Ser Asn Asp Phe Asp Ile Tyr Arg Leu Ser	450	455	460	
aat atg atg tct gct aag ggg tgg aat ttt aac tac ctg cag ttc cca				1440
Asn Met Met Ser Ala Lys Gly Trp Asn Phe Asn Tyr Leu Gln Phe Pro	465	470	475	480
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Arg Ser Ile His Phe Cys Ile Thr Leu Val His Thr Arg Lys Arg Val	485	490	495	
gcg atc cag ttc cta aag gat atc cgg gaa tca gtc aca caa atc atg				1536
Ala Ile Gln Phe Leu Lys Asp Ile Arg Glu Ser Val Thr Gln Ile Met	500	505	510	
aag aat cct aaa gct aag acc aca gga atg ggt gcc atc tat ggc atg				1584
Lys Asn Pro Lys Ala Lys Thr Thr Gly Met Gly Ala Ile Tyr Gly Met	515	520	525	
gcc cag gca acc att gac agg aag ctg gtt gca gaa ata tcc tcc gtc				1632
Ala Gln Ala Thr Ile Asp Arg Lys Leu Val Ala Glu Ile Ser Ser Val	530	535	540	
ttc ttg gac tgc ctt tat act acg gac ccc gtg act cag ggc aac cag				1680
Phe Leu Asp Cys Leu Tyr Thr Thr Asp Pro Val Thr Gln Gly Asn Gln	545	550	555	560
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Met Asn Gly Ser Pro Lys Pro Arg *	565			

<210> 6

<211> 568

<212> PRT

<213> Mus musculus

<400> 6

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Tyr Cys Thr Lys Tyr Glu Pro Trp Gln Leu Ile Ala Trp Ser Val Leu	35	40	45
Cys Thr Leu Leu Ile Val Trp Val Tyr Glu Leu Ile Phe Gln Pro Glu	50	55	60
Ser Leu Trp Ser Arg Phe Lys Lys Lys Leu Phe Lys Leu Ile Arg Lys	65	70	75
Met Pro Phe Ile Gly Arg Lys Ile Glu Gln Gln Val Ser Lys Ala Lys	85	90	95
Lys Asp Leu Val Lys Asn Met Pro Phe Leu Lys Val Asp Lys Asp Tyr	100	105	110
Val Lys Thr Leu Pro Ala Gln Gly Met Gly Thr Ala Glu Val Leu Glu	115	120	125
Arg Leu Lys Glu Tyr Ser Ser Met Asp Gly Ser Trp Gln Glu Gly Lys	130	135	140
Ala Ser Gly Ala Val Tyr Asn Gly Glu Pro Lys Leu Thr Glu Leu Leu	145	150	155
Val Gln Ala Tyr Gly Glu Phe Thr Trp Ser Asn Pro Leu His Pro Asp	165	170	175
Ile Phe Pro Gly Leu Arg Lys Leu Glu Ala Glu Ile Val Arg Met Thr	180	185	190
Cys Ser Leu Phe Asn Gly Gly Pro Asp Ser Cys Gly Cys Val Thr Ser	195	200	205
Gly Gly Thr Glu Ser Ile Leu Met Ala Cys Lys Ala Tyr Arg Asp Leu	210	215	220
Ala Leu Glu Lys Gly Ile Lys Thr Pro Glu Ile Val Ala Pro Glu Ser	225	230	235
Ala His Ala Ala Phe Asp Lys Ala Ala His Tyr Phe Gly Met Lys Ile	245	250	255
Val Arg Val Ala Leu Lys Lys Asn Met Glu Val Asp Val Gln Ala Met	260	265	270
Lys Arg Ala Ile Ser Arg Asn Thr Ala Met Leu Val Cys Ser Thr Pro	275	280	285
Gln Phe Pro His Gly Val Met Asp Pro Val Pro Glu Val Ala Lys Leu	290	295	300
Thr Val Arg Tyr Lys Ile Pro Leu His Val Asp Ala Cys Leu Gly Gly	305	310	315
Phe Leu Ile Val Phe Met Glu Lys Ala Gly Tyr Pro Leu Glu Lys Pro	325	330	335
Phe Asp Phe Arg Val Lys Gly Val Thr Ser Ile Ser Ala Asp Thr His	340	345	350
Lys Tyr Gly Tyr Ala Pro Lys Gly Ser Ser Val Val Met Tyr Ser Asn	355	360	365
Glu Lys Tyr Arg Thr Tyr Gln Phe Phe Val Gly Ala Asp Trp Gln Gly	370	375	380
Gly Val Tyr Ala Ser Pro Ser Ile Ala Gly Ser Arg Pro Gly Gly Ile	385	390	395
Ile Ala Ala Cys Trp Ala Ala Leu Met His Phe Gly Glu Asn Gly Tyr	405	410	415
Val Glu Ala Thr Lys Gln Ile Ile Lys Thr Ala Arg Phe Leu Lys Ser	420	425	430
Glu Leu Glu Asn Ile Lys Asn Ile Phe Ile Phe Gly Asp Pro Gln Leu			

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          435              440              445
Ser Val Ile Ala Leu Gly Ser Asn Asp Phe Asp Ile Tyr Arg Leu Ser
   450              455              460
Asn Met Met Ser Ala Lys Gly Trp Asn Phe Asn Tyr Leu Gln Phe Pro
465              470              475              480
Arg Ser Ile His Phe Cys Ile Thr Leu Val His Thr Arg Lys Arg Val
          485              490              495
Ala Ile Gln Phe Leu Lys Asp Ile Arg Glu Ser Val Thr Gln Ile Met
          500              505              510
Lys Asn Pro Lys Ala Lys Thr Thr Gly Met Gly Ala Ile Tyr Gly Met
          515              520              525
Ala Gln Ala Thr Ile Asp Arg Lys Leu Val Ala Glu Ile Ser Ser Val
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545              550              555              560
Met Asn Gly Ser Pro Lys Pro Arg
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<210> 7
<211> 1707
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (1)...(1707)

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Met Pro Ser Thr Asp Leu Leu Met Leu Lys Ala Phe Glu Pro Tyr Leu
 1              5              10              15

gag att ttg gaa gta tac tcc aca aaa gcc aag aat tat gta aat gga 96
Glu Ile Leu Glu Val Tyr Ser Thr Lys Ala Lys Asn Tyr Val Asn Gly
          20              25              30

cat tgc acc aag tat gag ccc tgg cag cta att gca tgg agt gtc gtg 144
His Cys Thr Lys Tyr Glu Pro Trp Gln Leu Ile Ala Trp Ser Val Val
          35              40              45

tgg acc ctg ctg ata gtc tgg gga tat gag ttt gtc ttc cag cca gag 192
Trp Thr Leu Leu Ile Val Trp Gly Tyr Glu Phe Val Phe Gln Pro Glu
          50              55              60

agt tta tgg tca agg ttt aaa aag aaa tgt ttt aag ctc acc agg aag 240
Ser Leu Trp Ser Arg Phe Lys Lys Lys Cys Phe Lys Leu Thr Arg Lys
65              70              75              80

atg ccc att att ggt cgt aag att caa gac aag ttg aac aag acc aag 288
Met Pro Ile Ile Gly Arg Lys Ile Gln Asp Lys Leu Asn Lys Thr Lys
          85              90              95

gat gat att agc aag aac atg tca ttc ctg aaa gtg gac aaa gag tat 336

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Asp	Asp	Ile	Ser	Lys	Asn	Met	Ser	Phe	Leu	Lys	Val	Asp	Lys	Glu	Tyr	
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gtg	aaa	gct	tta	ccc	tcc	cag	ggg	ctg	agc	tca	tct	gct	ggt	ttg	gag	384
Val	Lys	Ala	Leu	Pro	Ser	Gln	Gly	Leu	Ser	Ser	Ser	Ala	Val	Leu	Glu	
		115					120					125				
aaa	ctt	aag	gag	tac	agc	tct	atg	gac	gcc	ttc	tgg	caa	gag	ggg	aga	432
Lys	Leu	Lys	Glu	Tyr	Ser	Ser	Met	Asp	Ala	Phe	Trp	Gln	Glu	Gly	Arg	
	130					135					140					
gcc	tct	gga	aca	gtg	tac	agt	ggg	gag	gag	aag	ctc	act	gag	ctc	ctt	480
Ala	Ser	Gly	Thr	Val	Tyr	Ser	Gly	Glu	Glu	Lys	Leu	Thr	Glu	Leu	Leu	
145					150					155					160	
gtg	aag	gct	tat	gga	gat	ttt	gca	tgg	agt	aac	ccc	ctg	cat	cca	gat	528
Val	Lys	Ala	Tyr	Gly	Asp	Phe	Ala	Trp	Ser	Asn	Pro	Leu	His	Pro	Asp	
			165					170						175		
atc	ttc	cca	gga	cta	cgc	aag	ata	gag	gca	gaa	att	gtg	agg	ata	gct	576
Ile	Phe	Pro	Gly	Leu	Arg	Lys	Ile	Glu	Ala	Glu	Ile	Val	Arg	Ile	Ala	
			180					185					190			
tgt	tcc	ctg	ttc	aat	ggg	gga	cca	gat	tgc	tgt	gga	tgt	gtg	act	tct	624
Cys	Ser	Leu	Phe	Asn	Gly	Gly	Pro	Asp	Ser	Cys	Gly	Cys	Val	Thr	Ser	
		195					200					205				
ggg	gga	aca	gaa	agc	ata	ctc	atg	gcc	tgc	aaa	gca	tgt	cgg	gat	ctg	672
Gly	Gly	Thr	Glu	Ser	Ile	Leu	Met	Ala	Cys	Lys	Ala	Cys	Arg	Asp	Leu	
	210					215					220					
gcc	ttt	gag	aag	ggg	atc	aaa	act	cca	gaa	att	gtg	gct	ccc	caa	agt	720
Ala	Phe	Glu	Lys	Gly	Ile	Lys	Thr	Pro	Glu	Ile	Val	Ala	Pro	Gln	Ser	
225					230					235					240	
gcc	cat	gct	gca	ttt	aac	aaa	gca	gcc	agt	tac	ttt	ggg	atg	aag	att	768
Ala	His	Ala	Ala	Phe	Asn	Lys	Ala	Ala	Ser	Tyr	Phe	Gly	Met	Lys	Ile	
				245					250					255		
gtg	cgg	gtc	cca	ttg	acg	aag	atg	atg	gag	gtg	gat	gtg	agg	gca	atg	816
Val	Arg	Val	Pro	Leu	Thr	Lys	Met	Met	Glu	Val	Asp	Val	Arg	Ala	Met	
			260					265					270			
aga	aga	gct	atc	tcc	agg	aac	act	gcc	atg	ctc	gtc	tgt	tct	acc	cca	864
Arg	Arg	Ala	Ile	Ser	Arg	Asn	Thr	Ala	Met	Leu	Val	Cys	Ser	Thr	Pro	
		275					280					285				
cag	ttt	cct	cat	ggt	gta	ata	gat	cct	gtc	cct	gaa	gtg	gcc	aag	ctg	912
Gln	Phe	Pro	His	Gly	Val	Ile	Asp	Pro	Val	Pro	Glu	Val	Ala	Lys	Leu	
	290					295					300					
gct	gtc	aaa	tac	aaa	ata	ccc	ctt	cat	gtc	gac	gct	tgt	ctg	gga	ggc	960
Ala	Val	Lys	Tyr	Lys	Ile	Pro	Leu	His	Val	Asp	Ala	Cys	Leu	Gly	Gly	
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Phe Leu Ile Val Phe Met Glu Lys Ala Gly Tyr Pro Leu Glu His Pro	
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ttt gat ttc cgg gtg aaa ggt gta acc agc att tca gct gac acc cat	1056
Phe Asp Phe Arg Val Lys Gly Val Thr Ser Ile Ser Ala Asp Thr His	
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aag tat ggc tat gcc cca aaa ggc tca tca ttg gtg ttg tat agt gac	1104
Lys Tyr Gly Tyr Ala Pro Lys Gly Ser Ser Leu Val Leu Tyr Ser Asp	
355 360 365	
aag aag tac agg aac tat cag ttc ttc gtc gat aca gat tgg cag ggt	1152
Lys Lys Tyr Arg Asn Tyr Gln Phe Phe Val Asp Thr Asp Trp Gln Gly	
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ggc atc tat gct tcc cca acc atc gca ggc tca cgg cct ggt ggc att	1200
Gly Ile Tyr Ala Ser Pro Thr Ile Ala Gly Ser Arg Pro Gly Gly Ile	
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agc gca gcc tgt tgg gct gcc ttg atg cac ttc ggt gag aac ggc tat	1248
Ser Ala Ala Cys Trp Ala Ala Leu Met His Phe Gly Glu Asn Gly Tyr	
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gtt gaa gct acc aaa cag atc atc aaa act gct cgc ttc ctc aag tca	1296
Val Glu Ala Thr Lys Gln Ile Ile Lys Thr Ala Arg Phe Leu Lys Ser	
420 425 430	
gaa ctg gaa aat atc aaa ggc atc ttt gtt ttt ggg aat ccc caa ttg	1344
Glu Leu Glu Asn Ile Lys Gly Ile Phe Val Phe Gly Asn Pro Gln Leu	
435 440 445	
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Ser Leu Ile Ala Leu Gly Ser Arg Asp Phe Asp Ile Tyr Arg Leu Ser	
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Asn Leu Met Thr Ala Lys Gly Trp Asn Leu Asn Gln Leu Gln Phe Pro	
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Pro Ser Ile His Phe Cys Ile Thr Leu Leu His Ala Arg Lys Arg Val	
485 490 495	
gct ata caa ttc cta aag gac att cga gaa tct gtc act caa atc atg	1536
Ala Ile Gln Phe Leu Lys Asp Ile Arg Glu Ser Val Thr Gln Ile Met	
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Lys Asn Pro Lys Ala Lys Thr Thr Gly Met Gly Ala Ile Tyr Ala Met	
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gcc cag aca act gtt gac agg aat atg gtt gca gaa ttg tcc tca gtc	1632

Ala Gln Thr Thr Val Asp Arg Asn Met Val Ala Glu Leu Ser Ser Val
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ttc ttg gac agc ttg tac agc acc gac act gtc acc cag ggc agc cag 1680
 Phe Leu Asp Ser Leu Tyr Ser Thr Asp Thr Val Thr Gln Gly Ser Gln
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atg aat ggt tct cca aaa ccc cac tga 1707
 Met Asn Gly Ser Pro Lys Pro His *
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 <211> 568
 <212> PRT
 <213> Homo sapiens

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 Trp Thr Leu Leu Ile Val Trp Gly Tyr Glu Phe Val Phe Gln Pro Glu
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 Ser Leu Trp Ser Arg Phe Lys Lys Lys Cys Phe Lys Leu Thr Arg Lys
 65 70 75 80
 Met Pro Ile Ile Gly Arg Lys Ile Gln Asp Lys Leu Asn Lys Thr Lys
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 Asp Asp Ile Ser Lys Asn Met Ser Phe Leu Lys Val Asp Lys Glu Tyr
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 Val Lys Ala Leu Pro Ser Gln Gly Leu Ser Ser Ser Ala Val Leu Glu
 115 120 125
 Lys Leu Lys Glu Tyr Ser Ser Met Asp Ala Phe Trp Gln Glu Gly Arg
 130 135 140
 Ala Ser Gly Thr Val Tyr Ser Gly Glu Glu Lys Leu Thr Glu Leu Leu
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 Val Lys Ala Tyr Gly Asp Phe Ala Trp Ser Asn Pro Leu His Pro Asp
 165 170 175
 Ile Phe Pro Gly Leu Arg Lys Ile Glu Ala Glu Ile Val Arg Ile Ala
 180 185 190
 Cys Ser Leu Phe Asn Gly Gly Pro Asp Ser Cys Gly Cys Val Thr Ser
 195 200 205
 Gly Gly Thr Glu Ser Ile Leu Met Ala Cys Lys Ala Cys Arg Asp Leu
 210 215 220
 Ala Phe Glu Lys Gly Ile Lys Thr Pro Glu Ile Val Ala Pro Gln Ser
 225 230 235 240
 Ala His Ala Ala Phe Asn Lys Ala Ala Ser Tyr Phe Gly Met Lys Ile
 245 250 255
 Val Arg Val Pro Leu Thr Lys Met Met Glu Val Asp Val Arg Ala Met
 260 265 270
 Arg Arg Ala Ile Ser Arg Asn Thr Ala Met Leu Val Cys Ser Thr Pro
 275 280 285

Gln Phe Pro His Gly Val Ile Asp Pro Val Pro Glu Val Ala Lys Leu
 290 295 300
 Ala Val Lys Tyr Lys Ile Pro Leu His Val Asp Ala Cys Leu Gly Gly
 305 310 315 320
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 325 330 335
 Phe Asp Phe Arg Val Lys Gly Val Thr Ser Ile Ser Ala Asp Thr His
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 Lys Tyr Gly Tyr Ala Pro Lys Gly Ser Ser Leu Val Leu Tyr Ser Asp
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 Lys Lys Tyr Arg Asn Tyr Gln Phe Phe Val Asp Thr Asp Trp Gln Gly
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 Gly Ile Tyr Ala Ser Pro Thr Ile Ala Gly Ser Arg Pro Gly Gly Ile
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 Ser Ala Ala Cys Trp Ala Ala Leu Met His Phe Gly Glu Asn Gly Tyr
 405 410 415
 Val Glu Ala Thr Lys Gln Ile Ile Lys Thr Ala Arg Phe Leu Lys Ser
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 Glu Leu Glu Asn Ile Lys Gly Ile Phe Val Phe Gly Asn Pro Gln Leu
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 Ser Leu Ile Ala Leu Gly Ser Arg Asp Phe Asp Ile Tyr Arg Leu Ser
 450 455 460
 Asn Leu Met Thr Ala Lys Gly Trp Asn Leu Asn Gln Leu Gln Phe Pro
 465 470 475 480
 Pro Ser Ile His Phe Cys Ile Thr Leu Leu His Ala Arg Lys Arg Val
 485 490 495
 Ala Ile Gln Phe Leu Lys Asp Ile Arg Glu Ser Val Thr Gln Ile Met
 500 505 510
 Lys Asn Pro Lys Ala Lys Thr Thr Gly Met Gly Ala Ile Tyr Ala Met
 515 520 525
 Ala Gln Thr Thr Val Asp Arg Asn Met Val Ala Glu Leu Ser Ser Val
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<211> 1467

<212> DNA

<213> Homo sapiens

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<221> CDS

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 Glu Ile Leu Glu Val Tyr Ser Thr Lys Ala Lys Asn Tyr Val Asn Gly

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agt tta tgg tca agg ttt aaa aag aaa tgt ttt aag ctc acc agg aag Ser Leu Trp Ser Arg Phe Lys Lys Lys Cys Phe Lys Leu Thr Arg Lys 65 70 75 80			240
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gat gat att agc aag aac atg tca ttc ctg aaa gtg gac aaa gag tat Asp Asp Ile Ser Lys Asn Met Ser Phe Leu Lys Val Asp Lys Glu Tyr 100 105 110			336
gtg aaa gct tta ccc tcc cag ggt ctg agc tca tct gct gtt ttg gag Val Lys Ala Leu Pro Ser Gln Gly Leu Ser Ser Ser Ala Val Leu Glu 115 120 125			384
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gcc tct gga aca gtg tac agt ggg gag gag aag ctc act gag ctc ctt Ala Ser Gly Thr Val Tyr Ser Gly Glu Glu Lys Leu Thr Glu Leu Leu 145 150 155 160			480
gtg aag gct tat gga gat ttt gca tgg agt aac ccc ctg cat cca gat Val Lys Ala Tyr Gly Asp Phe Ala Trp Ser Asn Pro Leu His Pro Asp 165 170 175			528
atc ttc cca gga cta cgc aag ata gag gca gaa att gtg agg ata gct Ile Phe Pro Gly Leu Arg Lys Ile Glu Ala Glu Ile Val Arg Ile Ala 180 185 190			576
tgt tcc ctg ttc aat ggg gga cca gat tcg tgt gga tgt gtg act tct Cys Ser Leu Phe Asn Gly Gly Pro Asp Ser Cys Gly Cys Val Thr Ser 195 200 205			624
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gtg cgg gtc cca ttg acg aag atg atg gag gtg gat gtg agg gca atg	816
Val Arg Val Pro Leu Thr Lys Met Met Glu Val Asp Val Arg Ala Met	
260 265 270	
aga aga gct atc tcc agg aac act gcc atg ctc gtc tgt tct acc cca	864
Arg Arg Ala Ile Ser Arg Asn Thr Ala Met Leu Val Cys Ser Thr Pro	
275 280 285	
cag ttt cct cat ggt gta ata gat cct gtc cct gaa gtg gcc aag ctg	912
Gln Phe Pro His Gly Val Ile Asp Pro Val Pro Glu Val Ala Lys Leu	
290 295 300	
gct gtc aaa tac aaa ata ccc ctt cat gtc gac gct tgt ctg gga ggc	960
Ala Val Lys Tyr Lys Ile Pro Leu His Val Asp Ala Cys Leu Gly Gly	
305 310 315 320	
ttc ctc atc gtc ttt atg gag aaa gca gga tac cca ctg gag cac cca	1008
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Met Pro Ile Ile Gly Arg Lys Ile Gln Asp Lys Leu Asn Lys Thr Lys			
85 90 95			
gat gat att agc aag aac atg tca ttc ctg aaa gtg gac aaa gag tat	336		
Asp Asp Ile Ser Lys Asn Met Ser Phe Leu Lys Val Asp Lys Glu Tyr			
100 105 110			
gtg aaa gct tta ccc tcc cag ggt ctg agc tca tct gct gtt ttg gag	384		
Val Lys Ala Leu Pro Ser Gln Gly Leu Ser Ser Ser Ala Val Leu Glu			
115 120 125			
aaa ctt aag gag tac agc tct atg gac gcc ttc tgg caa gag ggg aga	432		
Lys Leu Lys Glu Tyr Ser Ser Met Asp Ala Phe Trp Gln Glu Gly Arg			
130 135 140			
gcc tct gga aca gtg tac agt ggg gag gag aag ctc act gag ctc ctt	480		
Ala Ser Gly Thr Val Tyr Ser Gly Glu Glu Lys Leu Thr Glu Leu Leu			
145 150 155 160			
gtg aag gct tat gga gat ttt gca tgg agt aac ccc ctg cat cca gat	528		
Val Lys Ala Tyr Gly Asp Phe Ala Trp Ser Asn Pro Leu His Pro Asp			
165 170 175			
atc ttc cca gga cta cgc aag ata gag gca gaa att gtg agg ata gct	576		
Ile Phe Pro Gly Leu Arg Lys Ile Glu Ala Glu Ile Val Arg Ile Ala			
180 185 190			
tgt tcc ctg ttc aat ggg gga cca gat tgc tgt gga tgt gtg act tct	624		
Cys Ser Leu Phe Asn Gly Gly Pro Asp Ser Cys Gly Cys Val Thr Ser			
195 200 205			
ggg gga aca gaa agc ata ctc atg gcc tgc aaa gca tat cgg gat ctg	672		
Gly Gly Thr Glu Ser Ile Leu Met Ala Cys Lys Ala Tyr Arg Asp Leu			
210 215 220			
gcc ttt gag aag ggg atc aaa act cca gaa att gtg gct ccc caa agt	720		
Ala Phe Glu Lys Gly Ile Lys Thr Pro Glu Ile Val Ala Pro Gln Ser			
225 230 235 240			
gcc cat gct gca ttt aac aaa gca gcc agt tac ttt ggg atg aag att	768		
Ala His Ala Ala Phe Asn Lys Ala Ala Ser Tyr Phe Gly Met Lys Ile			
245 250 255			
gtg cgg gtc cca ttg acg aag atg atg gag gtg gat gtg agg gca atg	816		
Val Arg Val Pro Leu Thr Lys Met Met Glu Val Asp Val Arg Ala Met			
260 265 270			

aga aga gct atc tcc agg aac act gcc atg ctc gtc tgt tct acc cca	864
Arg Arg Ala Ile Ser Arg Asn Thr Ala Met Leu Val Cys Ser Thr Pro	
275 280 285	
cag ttt cct cat ggt gta ata gat cct gtc cct gaa gtg gcc aag ctg	912
Gln Phe Pro His Gly Val Ile Asp Pro Val Pro Glu Val Ala Lys Leu	
290 295 300	
gct gtc aaa tac aaa ata ccc ctt cat gtc gac gct tgt ctg gga ggc	960
Ala Val Lys Tyr Lys Ile Pro Leu His Val Asp Ala Cys Leu Gly Gly	
305 310 315 320	
ttc ctc atc gtc ttt atg gag aaa gca gga tac cca ctg gag cac cca	1008
Phe Leu Ile Val Phe Met Glu Lys Ala Gly Tyr Pro Leu Glu His Pro	
325 330 335	
ttt gat ttc cgg gtg aaa ggt gta acc agc att tca gct gac acc cat	1056
Phe Asp Phe Arg Val Lys Gly Val Thr Ser Ile Ser Ala Asp Thr His	
340 345 350	
aag tat ggc tat gcc cca aaa ggc tca tca ttg gtg ttg tat agt gac	1104
Lys Tyr Gly Tyr Ala Pro Lys Gly Ser Ser Leu Val Leu Tyr Ser Asp	
355 360 365	
aag aag tac agg aac tat cag ttc ttc gtc gat aca gat tgg cag ggt	1152
Lys Lys Tyr Arg Asn Tyr Gln Phe Phe Val Asp Thr Asp Trp Gln Gly	
370 375 380	
ggc atc tat gct tcc cca acc atc gca ggc tca cgg cct ggt ggc att	1200
Gly Ile Tyr Ala Ser Pro Thr Ile Ala Gly Ser Arg Pro Gly Gly Ile	
385 390 395 400	
agc gca gcc tgt tgg gct gcc ttg atg cac ttc ggt gag aac ggc tat	1248
Ser Ala Ala Cys Trp Ala Ala Leu Met His Phe Gly Glu Asn Gly Tyr	
405 410 415	
gtt gaa gct acc aaa cag atc atc aaa act gct cgc ttc ctc aag tca	1296
Val Glu Ala Thr Lys Gln Ile Ile Lys Thr Ala Arg Phe Leu Lys Ser	
420 425 430	
gaa ctg gaa aat atc aaa ggc atc ttt gtt ttt ggg aat ccc caa ttg	1344
Glu Leu Glu Asn Ile Lys Gly Ile Phe Val Phe Gly Asn Pro Gln Leu	
435 440 445	
tca gtc att gct ctg gga tcc cgt gat ttt gac atc tac cga cta tca	1392
Ser Val Ile Ala Leu Gly Ser Arg Asp Phe Asp Ile Tyr Arg Leu Ser	
450 455 460	
aac ctg atg act gct aag ggg tgg aac ttg aac cag ttg cag ttc cca	1440
Asn Leu Met Thr Ala Lys Gly Trp Asn Leu Asn Gln Leu Gln Phe Pro	
465 470 475 480	
ccc agt att cat ttc tgc atc aca tta cta cac gcc cgg aaa cga gta	1488
Pro Ser Ile His Phe Cys Ile Thr Leu Leu His Ala Arg Lys Arg Val	

485										490					495					
gct	ata	caa	ttc	cta	aag	gac	att	cga	gaa	tct	gtc	act	caa	atc	atg	1536				
Ala	Ile	Gln	Phe	Leu	Lys	Asp	Ile	Arg	Glu	Ser	Val	Thr	Gln	Ile	Met					
			500					505					510							
aag	aat	cct	aaa	gcg	aag	acc	aca	gga	atg	ggg	gcc	atc	tat	ggc	atg	1584				
Lys	Asn	Pro	Lys	Ala	Lys	Thr	Thr	Gly	Met	Gly	Ala	Ile	Tyr	Gly	Met					
		515					520					525								
gcc	cag	aca	act	gtt	gac	agg	aat	atg	gtt	gca	gaa	ttg	tcc	tca	gtc	1632				
Ala	Gln	Thr	Thr	Val	Asp	Arg	Asn	Met	Val	Ala	Glu	Leu	Ser	Ser	Val					
	530					535					540									
ttc	ttg	gac	agc	ttg	tac	agc	acc	gac	act	gtc	acc	cag	ggc	agc	cag	1680				
Phe	Leu	Asp	Ser	Leu	Tyr	Ser	Thr	Asp	Thr	Val	Thr	Gln	Gly	Ser	Gln					
545					550					555					560					
atg	aat	ggg	tct	cca	aaa	ccc	cac	tga								1707				
Met	Asn	Gly	Ser	Pro	Lys	Pro	His	*												
				565																

<210> 18

<211> 568

<212> PRT

<213> Homo sapiens

<400> 18

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Glu	Ile	Leu	Glu	Val	Tyr	Ser	Thr	Lys	Ala	Lys	Asn	Tyr	Val	Asn	Gly	
			20					25					30			
His	Cys	Thr	Lys	Tyr	Glu	Pro	Trp	Gln	Leu	Ile	Ala	Trp	Ser	Val	Val	
		35					40					45				
Trp	Thr	Leu	Leu	Ile	Val	Trp	Gly	Tyr	Glu	Phe	Val	Phe	Gln	Pro	Glu	
	50					55					60					
Ser	Leu	Trp	Ser	Arg	Phe	Lys	Lys	Lys	Cys	Phe	Lys	Leu	Thr	Arg	Lys	
65				70					75					80		
Met	Pro	Ile	Ile	Gly	Arg	Lys	Ile	Gln	Asp	Lys	Leu	Asn	Lys	Thr	Lys	
				85				90					95			
Asp	Asp	Ile	Ser	Lys	Asn	Met	Ser	Phe	Leu	Lys	Val	Asp	Lys	Glu	Tyr	
		100					105						110			
Val	Lys	Ala	Leu	Pro	Ser	Gln	Gly	Leu	Ser	Ser	Ser	Ala	Val	Leu	Glu	
		115				120						125				
Lys	Leu	Lys	Glu	Tyr	Ser	Ser	Met	Asp	Ala	Phe	Trp	Gln	Glu	Gly	Arg	
	130					135					140					
Ala	Ser	Gly	Thr	Val	Tyr	Ser	Gly	Glu	Glu	Lys	Leu	Thr	Glu	Leu	Leu	
145					150					155					160	
Val	Lys	Ala	Tyr	Gly	Asp	Phe	Ala	Trp	Ser	Asn	Pro	Leu	His	Pro	Asp	
				165				170						175		
Ile	Phe	Pro	Gly	Leu	Arg	Lys	Ile	Glu	Ala	Glu	Ile	Val	Arg	Ile	Ala	
			180					185					190			
Cys	Ser	Leu	Phe	Asn	Gly	Gly	Pro	Asp	Ser	Cys	Gly	Cys	Val	Thr	Ser	

		195					200					205					
Gly	Gly	Thr	Glu	Ser	Ile	Leu	Met	Ala	Cys	Lys	Ala	Tyr	Arg	Asp	Leu		
	210					215					220						
Ala	Phe	Glu	Lys	Gly	Ile	Lys	Thr	Pro	Glu	Ile	Val	Ala	Pro	Gln	Ser		
225					230					235					240		
Ala	His	Ala	Ala	Phe	Asn	Lys	Ala	Ala	Ser	Tyr	Phe	Gly	Met	Lys	Ile		
				245					250					255			
Val	Arg	Val	Pro	Leu	Thr	Lys	Met	Met	Glu	Val	Asp	Val	Arg	Ala	Met		
			260					265						270			
Arg	Arg	Ala	Ile	Ser	Arg	Asn	Thr	Ala	Met	Leu	Val	Cys	Ser	Thr	Pro		
		275					280						285				
Gln	Phe	Pro	His	Gly	Val	Ile	Asp	Pro	Val	Pro	Glu	Val	Ala	Lys	Leu		
	290					295					300						
Ala	Val	Lys	Tyr	Lys	Ile	Pro	Leu	His	Val	Asp	Ala	Cys	Leu	Gly	Gly		
305					310					315					320		
Phe	Leu	Ile	Val	Phe	Met	Glu	Lys	Ala	Gly	Tyr	Pro	Leu	Glu	His	Pro		
				325					330					335			
Phe	Asp	Phe	Arg	Val	Lys	Gly	Val	Thr	Ser	Ile	Ser	Ala	Asp	Thr	His		
			340					345					350				
Lys	Tyr	Gly	Tyr	Ala	Pro	Lys	Gly	Ser	Ser	Leu	Val	Leu	Tyr	Ser	Asp		
	355					360						365					
Lys	Lys	Tyr	Arg	Asn	Tyr	Gln	Phe	Phe	Val	Asp	Thr	Asp	Trp	Gln	Gly		
	370					375					380						
Gly	Ile	Tyr	Ala	Ser	Pro	Thr	Ile	Ala	Gly	Ser	Arg	Pro	Gly	Gly	Ile		
385					390					395					400		
Ser	Ala	Ala	Cys	Trp	Ala	Ala	Leu	Met	His	Phe	Gly	Glu	Asn	Gly	Tyr		
			405					410						415			
Val	Glu	Ala	Thr	Lys	Gln	Ile	Ile	Lys	Thr	Ala	Arg	Phe	Leu	Lys	Ser		
			420					425					430				
Glu	Leu	Glu	Asn	Ile	Lys	Gly	Ile	Phe	Val	Phe	Gly	Asn	Pro	Gln	Leu		
		435				440						445					
Ser	Val	Ile	Ala	Leu	Gly	Ser	Arg	Asp	Phe	Asp	Ile	Tyr	Arg	Leu	Ser		
	450				455						460						
Asn	Leu	Met	Thr	Ala	Lys	Gly	Trp	Asn	Leu	Asn	Gln	Leu	Gln	Phe	Pro		
465					470					475					480		
Pro	Ser	Ile	His	Phe	Cys	Ile	Thr	Leu	Leu	His	Ala	Arg	Lys	Arg	Val		
			485					490						495			
Ala	Ile	Gln	Phe	Leu	Lys	Asp	Ile	Arg	Glu	Ser	Val	Thr	Gln	Ile	Met		
			500					505					510				
Lys	Asn	Pro	Lys	Ala	Lys	Thr	Thr	Gly	Met	Gly	Ala	Ile	Tyr	Gly	Met		
		515				520						525					
Ala	Gln	Thr	Thr	Val	Asp	Arg	Asn	Met	Val	Ala	Glu	Leu	Ser	Ser	Val		
	530					535					540						
Phe	Leu	Asp	Ser	Leu	Tyr	Ser	Thr	Asp	Thr	Val	Thr	Gln	Gly	Ser	Gln		
545					550					555					560		
Met	Asn	Gly	Ser	Pro	Lys	Pro	His										
				565													

<210> 19

<211> 490

<212> PRT

<213> Drosophila melanogaster

<400> 19

Phe	Arg	Ser	Ser	Asn	Asp	Tyr	Gly	Val	Asn	Leu	Gln	Thr	Ala	Glu	Met
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Trp	His	His	Thr	Ile	Arg	Lys	His	Lys	Arg	Gly	Asn	Gly	Ser	Ser	Ser
			20					25					30		
Pro	Ala	Asp	Cys	Gly	Lys	Gln	Leu	Leu	Ile	Leu	Leu	Asn	Pro	Lys	Ser
		35					40					45			
Gly	Ser	Gly	Lys	Gly	Arg	Glu	Leu	Phe	Gln	Lys	Gln	Val	Ala	Pro	Leu
	50					55					60				
Leu	Thr	Glu	Ala	Glu	Val	Gln	Tyr	Asp	Leu	Gln	Ile	Thr	Thr	His	Pro
65					70					75					80
Gln	Tyr	Ala	Lys	Glu	Phe	Val	Arg	Thr	Arg	Arg	Asp	Leu	Leu	Thr	Arg
			85						90					95	
Tyr	Ser	Gly	Ile	Val	Val	Ala	Ser	Gly	Asp	Gly	Leu	Phe	Tyr	Glu	Val
			100					105					110		
Leu	Asn	Gly	Leu	Met	Glu	Arg	Met	Asp	Trp	Arg	Arg	Ala	Cys	Arg	Glu
	115						120					125			
Leu	Pro	Leu	Gly	Ile	Ile	Pro	Cys	Gly	Ser	Gly	Asn	Gly	Leu	Ala	Lys
	130					135					140				
Ser	Val	Ala	His	His	Cys	Asn	Glu	Pro	Tyr	Glu	Pro	Lys	Pro	Ile	Leu
145					150					155					160
His	Ala	Thr	Leu	Thr	Cys	Met	Ala	Gly	Lys	Ser	Thr	Pro	Met	Asp	Val
			165						170					175	
Val	Arg	Val	Glu	Leu	Ala	Thr	Arg	Asp	Lys	His	Phe	Val	Met	Tyr	Ser
			180					185					190		
Phe	Leu	Ser	Val	Gly	Trp	Gly	Leu	Ile	Ala	Asp	Ile	Asp	Ile	Glu	Ser
	195					200					205				
Glu	Arg	Leu	Arg	Ser	Ile	Gly	Ala	Gln	Arg	Phe	Thr	Leu	Trp	Ala	Ile
	210					215					220				
Lys	Arg	Leu	Ile	Gly	Leu	Arg	Ser	Tyr	Lys	Gly	Arg	Val	Ser	Tyr	Leu
225					230					235					240
Leu	Gly	Lys	Gly	Lys	Lys	Glu	Pro	Pro	Val	Glu	Ala	Ala	Arg	Glu	Leu
			245						250					255	
Pro	Ala	Glu	Ser	Thr	Ala	Ala	Gly	Ile	Arg	Ser	Ser	Leu	Pro	Leu	Asn
		260					265						270		
Ala	Gly	Glu	Phe	His	Asp	Leu	Pro	Glu	Glu	Glu	Glu	Gly	Glu	Ala	Val
	275					280						285			
Leu	Asp	Gly	Glu	Gln	Phe	Ala	Asp	Ala	Ile	Ser	Leu	Asp	Arg	Ser	Val
	290					295					300				
Tyr	Arg	Gln	His	Ala	Asp	Ser	Trp	His	Ser	Ala	Met	Ser	Arg	Arg	Thr
305					310					315					320
Ala	Tyr	Tyr	Ser	Leu	Gly	Gly	Pro	Ser	Met	Arg	Ser	Asn	Arg	Ser	Arg
			325						330					335	
Met	Ser	Ile	Ser	Gln	Arg	Ile	Glu	Ala	Ala	Asn	Ala	Glu	Phe	Ala	Glu
		340					345						350		
Arg	Val	Pro	Thr	Gly	Thr	Ile	Pro	Pro	Leu	Gln	Met	Pro	Leu	Leu	Ser
		355					360					365			
Ser	Asp	Gly	Trp	Ile	Cys	Glu	Asp	Gly	Asp	Phe	Val	Met	Val	His	Ala
	370					375					380				
Ala	Tyr	Thr	Thr	His	Leu	Ser	Ser	Asp	Val	Phe	Phe	Ala	Pro	Glu	Ser
385					390					395					400
Arg	Leu	Asp	Asp	Gly	Leu	Ile	Tyr	Leu	Val	Ile	Ile	Arg	Arg	Gly	Val
			405						410					415	
Ser	Arg	His	Gln	Leu	Leu	Asn	Phe	Met	Leu	Asn	Leu	Asn	Ala	Gly	Thr

420 425 430
 His Leu Pro Ile Gly Glu Asp Pro Phe Ile Lys Val Val Pro Cys Arg
 435 440 445
 Ala Phe Arg Ile Glu Pro Ser Ser Ser Asp Gly Ile Leu Val Val Asp
 450 455 460
 Gly Glu Arg Val Glu Tyr Gly Pro Ile Gln Ala Glu Val Met Pro Gly
 465 470 475 480
 Leu Ile Asn Val Met Thr Thr Ser Gly Gln
 485 490

<210> 20
 <211> 524
 <212> PRT
 <213> Drosophila melanogaster

<400> 20
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 Trp Tyr Arg Ser Leu Arg Trp Gln Leu His Arg Thr Leu Glu Glu Ile
 20 25 30
 Phe Val Ala Pro Thr Val Asp Glu Arg Arg Arg Arg Val Leu Val Leu
 35 40 45
 Leu Asn Pro Lys Ser Gly Ser Gly Asp Ala Arg Glu Val Phe Asn Met
 50 55 60
 His Val Thr Pro Val Leu Asn Glu Ala Glu Val Pro Tyr Asp Leu Tyr
 65 70 75 80
 Val Thr Lys His Ser Asn Phe Ala Ile Glu Phe Leu Ser Thr Arg Cys
 85 90 95
 Leu Asp Ala Trp Cys Cys Val Val Ala Val Gly Gly Asp Gly Leu Phe
 100 105 110
 His Glu Ile Val Asn Gly Leu Leu Gln Arg Gln Asp Trp Ala His Val
 115 120 125
 Leu Pro His Leu Ala Leu Gly Ile Ile Pro Cys Gly Ser Gly Asn Gly
 130 135 140
 Leu Ala Arg Ser Ile Ala His Cys Tyr Asn Lys Pro Val Leu Gly Ala
 145 150 155 160
 Ala Leu Thr Val Ile Ser Gly Arg Ser Ser Pro Met Asp Val Val Arg
 165 170 175
 Val Gln Leu Gln Ser Arg Ser Leu Tyr Ser Phe Leu Ser Ile Gly Trp
 180 185 190
 Gly Leu Ile Ser Asp Val Asp Ile Glu Ser Glu Arg Ile Arg Met Leu
 195 200 205
 Gly Tyr Gln Arg Phe Thr Val Trp Thr Leu Tyr Arg Leu Val Asn Leu
 210 215 220
 Arg Thr Tyr Asn Gly Arg Ile Ser Tyr Leu Leu Thr Asp His Glu Val
 225 230 235 240
 Ser Ser Thr His Ser Ala Thr Gly Tyr Ala Ala Gln Arg Arg Met Gln
 245 250 255
 Ser Ser Arg Ser Cys Asn Thr His Ile Asp Met Leu Asn Gly Pro Ala
 260 265 270
 Pro Ile Tyr His Ser Ser Ala Glu Tyr Leu Pro Gln Glu Phe Ala Asp
 275 280 285
 Val Ile Ser Leu Glu Thr Ser Ile Asn Gln Ser Phe Arg Ser Arg Cys

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      290              295              300
Asp Ser Trp Leu Ser Gly Gly Ser Arg Arg Ser Phe Tyr Tyr Ser Ile
305              310              315              320
Ser Glu Ser Ile Tyr His Ser Leu Ala Asp Glu Ser Glu Phe Ala Gly
      325              330              335
Leu Ala Ala Ala Ser Leu Glu Asn Arg Gln Gln Asn Tyr Gly Pro Ala
      340              345              350
Ser Glu Leu Pro Asp Leu Asn Glu Pro Leu Ser Glu Asp Gln Gly Trp
      355              360              365
Leu Val Glu Glu Gly Glu Phe Val Met Met His Ala Val Tyr Gln Thr
      370              375              380
His Leu Gly Ile Asp Cys His Phe Ala Pro Lys Ala Gln Leu Asn Asp
385              390              395              400
Gly Thr Ile Tyr Leu Ile Leu Ile Arg Ala Gly Ile Ser Arg Pro His
      405              410              415
Leu Leu Ser Phe Leu Tyr Asn Met Ser Ser Gly Thr His Leu Pro Glu
      420              425              430
Ser His Asp Asp His Val Lys Val Leu Pro Val Arg Ala Phe Arg Leu
      435              440              445
Glu Pro Tyr Asp Asn His Gly Ile Ile Thr Val Asp Gly Glu Arg Val
      450              455              460
Glu Phe Gly Pro Leu Gln Ala Glu Val Leu Pro Gly Ile Ala Arg Val
465              470              475              480
Met Val Pro Asn Val Ser Thr Phe Arg Phe Gln Ser Ala Thr Leu Gln
      485              490              495
His Gly Ile Pro Val Cys Ile Pro Val Arg Lys Arg Phe Val Leu Tyr
      500              505              510
Asn Met Ser Ser Glu Glu Leu Ala Pro Ile Asn Glu
      515              520

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<210> 21
<211> 368
<212> PRT
<213> Homo sapiens

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<400> 21
Val Leu Val Leu Leu Asn Pro Arg Gly Gly Lys Gly Lys Ala Leu Gln
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Leu Phe Arg Ser His Val Gln Pro Leu Leu Ala Glu Ala Glu Ile Ser
      20              25              30
Phe Thr Leu Met Leu Thr Glu Arg Arg Asn His Ala Arg Glu Leu Val
      35              40              45
Arg Ser Glu Glu Leu Gly Arg Trp Asp Ala Leu Val Val Met Ser Gly
      50              55              60
Asp Gly Leu Met His Glu Val Val Asn Gly Leu Met Glu Arg Pro Asp
      65              70              75              80
Trp Glu Thr Ala Ile Gln Lys Pro Leu Cys Ser Leu Pro Ala Gly Ser
      85              90              95
Gly Asn Ala Leu Ala Ala Ser Leu Asn His Tyr Ala Gly Tyr Glu Gln
      100              105              110
Val Thr Asn Glu Asp Leu Leu Thr Asn Cys Thr Leu Leu Leu Cys Arg
      115              120              125
Arg Leu Leu Ser Pro Met Asn Leu Leu Ser Leu His Thr Ala Ser Gly

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130		135		140
Leu Arg Leu Phe Ser Val	Leu Ser Leu Ala Trp Gly Phe Ile Ala Asp			
145	150	155	160	
Val Asp Leu Glu Ser Glu Lys Tyr Arg Arg Leu Gly Glu Met Arg Phe				
	165	170	175	
Thr Leu Gly Thr Phe Leu Arg Leu Ala Ala Leu Arg Thr Tyr Arg Gly				
	180	185	190	
Arg Leu Ala Tyr Leu Pro Val Gly Arg Val Gly Ser Lys Thr Pro Ala				
	195	200	205	
Ser Pro Val Val Val Gln Gln Gly Pro Val Asp Ala His Leu Val Pro				
	210	215	220	
Leu Glu Glu Pro Val Pro Ser His Trp Thr Val Val Pro Asp Glu Asp				
225	230	235	240	
Phe Val Leu Val Leu Ala Leu Leu His Ser His Leu Gly Ser Glu Met				
	245	250	255	
Phe Ala Ala Pro Met Gly Arg Cys Ala Ala Gly Val Met His Leu Phe				
	260	265	270	
Tyr Val Arg Ala Gly Val Ser Arg Ala Met Leu Leu Arg Leu Phe Leu				
	275	280	285	
Ala Met Glu Lys Gly Arg His Met Glu Tyr Glu Cys Pro Tyr Leu Val				
	290	295	300	
Tyr Val Pro Val Val Ala Phe Arg Leu Glu Pro Lys Asp Gly Lys Gly				
305	310	315	320	
Val Phe Ala Val Asp Gly Glu Leu Met Val Ser Glu Ala Val Gln Gly				
	325	330	335	
Gln Val His Pro Asn Tyr Phe Trp Met Val Ser Gly Cys Val Glu Pro				
	340	345	350	
Pro Pro Ser Trp Lys Pro Gln Gln Met Pro Pro Pro Glu Glu Pro Leu				
	355	360	365	

<210> 22
 <211> 1152
 <212> DNA
 <213> Homo sapiens

<400> 22
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 cttttggctg aggctgaaat ctccctcacg ctgatgctca ctgagcggcg gaaccacgcg 180
 cgggagctgg tgcggtcgga ggagctgggc cgctgggacg ctctggtggt catgtctgga 240
 gacgggctga tgcacgaggt ggtgaacggg ctcatggagc ggctgactg ggagaccgcc 300
 atccagaagc ccctgtgtag cctcccagca ggctctggca acgcgctggc agcttccttg 360
 aaccattatg ctggctatga gcaggtcacc aatgaagacc tctgaccaa ctgcacgcta 420
 ttgctgtgcc gccggctgct gtcacccatg aacctgctgt ctctgcacac ggcttcgggg 480
 ctgcgcctct tctctgtgct cagcctggcc tggggcttca ttgctgatgt ggacctagag 540
 agtgagaagt atcggcgctc gggggagatg cgcttactc tgggcacctt cctgcgtctg 600
 gcagccctgc gcacctaccg cggccgactg gcctacctc ctgtaggaag agtgggttcc 660
 aagacacctg cctcccccg tgtggtccag cagggcccg tagatgcaca ccttgtgcca 720
 ctggaggagc cagtgcctc tcaactggaca gtggtgcccg acgaggactt tgtgctagtc 780
 ctggcactgc tgcactcgca cctgggcagt gagatgtttg ctgcacccat gggccgctgt 840
 gcagctggcg tcatgcatct gttctacgtg cgggcgggag tgtctcgtgc catgctgctg 900
 cgcctcttcc tggccatgga gaagggcagg catatggagt atgaatgcc ctacttggtg 960
 tatgtgcccg tggctgcctt ccgcttgag cccaaggatg ggaaaggtgt gtttgacgtg 1020

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gatggggaat tgatggttag cgaggccgtg cagggccagg tgcacccaaa ctactttctgg 1080
atggtcagtg gttgcgtgga gcccccgccc agctggaagc cccagcagat gccaccgcca 1140
gaagagccct ta                                     1152

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<210> 23
<211> 1707
<212> DNA
<213> Homo sapiens

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<210> 24
<211> 2629
<212> DNA
<213> Drosophila melanogaster

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<210> 25

<211> 2609

<212> DNA

<213> *Drosophila melanogaster*

<400> 25

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<210> 26

<211> 2043

<212> DNA

<213> *Drosophila melanogaster*

<400> 26

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<210> 27

<211> 2043

<212> DNA

<213> *Drosophila melanogaster*

<400> 27

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<210> 28

<211> 641

<212> PRT

<213> *Drosophila melanogaster*

<400> 28

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Ser Gly Thr Pro Thr Glu Leu Ser Glu Ile Phe Phe Val Asp Asn Ser
          35          40          45
Arg Arg Lys Gln Ser Ile Lys Ile Gln Val Lys Leu Cys Pro Glu Gly
          50          55          60
Val Tyr Leu Arg Arg Glu Thr Glu Glu Asp Asp His Ile Asn Glu Gln
          65          70          75          80
Leu Ile Arg Ile Asp Asp Ile Ile Gly Ser Arg Tyr Gly Arg Arg Leu
          85          90          95
Lys Lys Arg Ala Arg Gly Gly Leu Asn Ser Cys Arg Asn Pro Asn Val
          100          105          110
Pro Gly Gln Glu Ala Asp Ser Glu Pro Asp Ser Asp Asn Ser Ala Tyr
          115          120          125
Leu Tyr Ile Tyr Ala Tyr Leu Lys Lys Glu Lys Pro Leu Arg Arg Val
          130          135          140
Gln Thr Leu Arg Ile Leu Arg Phe Arg Ser Ser Asn Asp Tyr Gly Val
          145          150          155          160
Asn Leu Gln Thr Ala Glu Met Trp His His Thr Ile Arg Lys His Lys
          165          170          175
Arg Gly Asn Gly Ser Ser Ser Pro Ala Asp Cys Gly Lys Gln Leu Leu
          180          185          190
Ile Leu Leu Asn Pro Lys Ser Gly Ser Gly Lys Gly Arg Glu Leu Phe
          195          200          205
Gln Lys Gln Val Ala Pro Leu Leu Thr Glu Ala Glu Val Gln Tyr Asp
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Leu Gln Ile Thr Thr His Pro Gln Tyr Ala Lys Glu Phe Val Arg Thr
          225          230          235          240
Arg Arg Asp Leu Leu Thr Arg Tyr Ser Gly Ile Val Val Ala Ser Gly
          245          250          255
Asp Gly Leu Phe Tyr Glu Val Leu Asn Gly Leu Met Glu Arg Met Asp
          260          265          270
Trp Arg Arg Ala Cys Arg Glu Leu Pro Leu Gly Ile Ile Pro Cys Gly
          275          280          285
Ser Gly Asn Gly Leu Ala Lys Ser Val Ala His His Cys Asn Glu Pro
          290          295          300

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Tyr Glu Pro Lys Pro Ile Leu His Ala Thr Leu Thr Cys Met Ala Gly
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 325 330 335
 Lys His Phe Val Met Tyr Ser Phe Leu Ser Val Gly Trp Gly Leu Ile
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 Ala Asp Ile Asp Ile Glu Ser Glu Arg Leu Arg Ser Ile Gly Ala Gln
 355 360 365
 Arg Phe Thr Leu Trp Ala Ile Lys Arg Leu Ile Gly Leu Arg Ser Tyr
 370 375 380
 Lys Gly Arg Val Ser Tyr Leu Leu Gly Lys Gly Lys Lys Glu Pro Pro
 385 390 395 400
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 Arg Ser Ser Leu Pro Leu Asn Ala Gly Glu Phe His Asp Leu Pro Glu
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 Glu Glu Glu Gly Glu Ala Val Leu Asp Gly Glu Gln Phe Ala Asp Ala
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 Ile Ser Leu Asp Arg Ser Val Tyr Arg Gln His Ala Asp Ser Trp His
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 565 570 575
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 580 585 590
 Ile Lys Val Val Pro Cys Arg Ala Phe Arg Ile Glu Pro Ser Ser Ser
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<210> 29

<211> 907

<212> PRT

<213> *Drosophila melanogaster*

<400> 29

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Ser	Asp	Thr	Phe	Tyr	Thr	Ser	Gln	Arg	Lys	Lys	Gly	Ser	His	Val	Phe	35	40	45
Arg	Val	Arg	Leu	Asp	Ala	Thr	Gly	Phe	Thr	Leu	Gln	Arg	Glu	Ser	Pro	50	55	60
Gly	Gly	Ser	Ile	Val	Lys	Glu	Gln	His	Val	Arg	Ile	Ser	Asp	Ile	Val	65	70	75
Gly	Ala	Arg	Cys	Met	Arg	Pro	Lys	Lys	Ser	Arg	Arg	Leu	Ala	Met	Ser	85	90	95
Gly	Ala	Cys	Ala	Cys	Ser	Ser	Gly	Asn	Pro	Asn	Ser	Pro	Ala	Ile	Ser	100	105	110
Ala	Ser	Gly	Asp	His	His	Arg	Pro	Ala	Thr	Thr	Pro	Ser	Lys	Cys	Ser	115	120	125
Thr	Asn	Ser	Arg	Asp	Asn	Ile	Pro	Ser	Asp	Gly	Gly	Asp	Val	Ser	Ala	130	135	140
Phe	Leu	Tyr	Val	Phe	Ala	Tyr	Val	Leu	Lys	Lys	Arg	Ser	Leu	Arg	Ser	145	150	155
Glu	Leu	His	Arg	Glu	Arg	Thr	Val	Leu	Thr	Leu	Arg	Phe	Arg	Ser	Phe	165	170	175
Asp	Thr	Phe	Glu	Asp	Asn	Met	Arg	Glu	Ala	Asp	Arg	Trp	Tyr	Arg	Ser	180	185	190
Leu	Arg	Trp	Gln	Leu	His	Arg	Thr	Leu	Glu	Glu	Ile	Phe	Val	Ala	Pro	195	200	205
Thr	Val	Asp	Glu	Arg	Arg	Arg	Arg	Val	Leu	Val	Leu	Leu	Asn	Pro	Lys	210	215	220
Ser	Gly	Ser	Gly	Asp	Ala	Arg	Glu	Val	Phe	Asn	Met	His	Val	Thr	Pro	225	230	235
Val	Leu	Asn	Glu	Ala	Glu	Val	Pro	Tyr	Asp	Leu	Tyr	Val	Thr	Lys	His	245	250	255
Ser	Asn	Phe	Ala	Ile	Glu	Phe	Leu	Ser	Thr	Arg	Cys	Leu	Asp	Ala	Trp	260	265	270
Cys	Cys	Val	Val	Ala	Val	Gly	Gly	Asp	Gly	Leu	Phe	His	Glu	Ile	Val	275	280	285
Asn	Gly	Leu	Leu	Gln	Arg	Gln	Asp	Trp	Ala	His	Val	Leu	Pro	His	Leu	290	295	300
Ala	Leu	Gly	Ile	Ile	Pro	Cys	Gly	Ser	Gly	Asn	Gly	Leu	Ala	Arg	Ser	305	310	315
Ile	Ala	His	Cys	Tyr	Asn	Lys	Pro	Val	Leu	Gly	Ala	Ala	Leu	Thr	Val	325	330	335
Ile	Ser	Gly	Arg	Ser	Ser	Pro	Met	Asp	Val	Val	Arg	Val	Gln	Leu	Gln	340	345	350
Ser	Arg	Ser	Leu	Tyr	Ser	Phe	Leu	Ser	Ile	Gly	Trp	Gly	Leu	Ile	Ser	355	360	365
Asp	Val	Asp	Ile	Glu	Ser	Glu	Arg	Ile	Arg	Met	Leu	Gly	Tyr	Gln	Arg	370	375	380
Phe	Thr	Val	Trp	Thr	Leu	Tyr	Arg	Leu	Val	Asn	Leu	Arg	Thr	Tyr	Asn	385	390	395
Gly	Arg	Ile	Ser	Tyr	Leu	Leu	Thr	Asp	His	Glu	Val	Ser	Ser	Thr	His	405	410	415
Ser	Ala	Thr	Gly	Tyr	Ala	Ala	Gln	Arg	Arg	Met	Gln	Ser	Ser	Arg	Ser	420	425	430
Cys	Asn	Thr	His	Ile	Asp	Met	Leu	Asn	Gly	Pro	Ala	Pro	Ile	Tyr	His	435	440	445

Ser	Ser	Ala	Glu	Tyr	Leu	Pro	Gln	Glu	Phe	Ala	Asp	Val	Ile	Ser	Leu
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465					470					475					480
Ser	Gly	Gly	Ser	Arg	Arg	Ser	Phe	Tyr	Tyr	Ser	Ile	Ser	Glu	Ser	Ile
				485				490						495	
Tyr	His	Ser	Leu	Ala	Asp	Glu	Ser	Glu	Phe	Ala	Gly	Leu	Ala	Ala	Ala
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Ser	Leu	Glu	Asn	Arg	Gln	Gln	Asn	Tyr	Gly	Pro	Ala	Ser	Glu	Leu	Pro
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Gly	Glu	Phe	Val	Met	Met	His	Ala	Val	Tyr	Gln	Thr	His	Leu	Gly	Ile
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Asp	Cys	His	Phe	Ala	Pro	Lys	Ala	Gln	Leu	Asn	Asp	Gly	Thr	Ile	Tyr
			565						570					575	
Leu	Ile	Leu	Ile	Arg	Ala	Gly	Ile	Ser	Arg	Pro	His	Leu	Leu	Ser	Phe
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Leu	Tyr	Asn	Met	Ser	Ser	Gly	Thr	His	Leu	Pro	Glu	Ser	His	Asp	Asp
		595					600					605			
His	Val	Lys	Val	Leu	Pro	Val	Arg	Ala	Phe	Arg	Leu	Glu	Pro	Tyr	Asp
	610					615					620				
Asn	His	Gly	Ile	Ile	Thr	Val	Asp	Gly	Glu	Arg	Val	Glu	Phe	Gly	Pro
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Leu	Gln	Ala	Glu	Val	Leu	Pro	Gly	Ile	Ala	Arg	Val	Met	Val	Pro	Asn
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Val	Cys	Ile	Pro	Val	Arg	Lys	Arg	Phe	Val	Leu	Tyr	Asn	Met	Ser	Ser
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Glu	Glu	Leu	Ala	Pro	Ile	Asn	Glu	Gln	Asp	Phe	Lys	Asp	Leu	Lys	Glu
	690					695					700				
Arg	Met	Lys	Leu	Ile	Val	Glu	Ala	Asp	Pro	Lys	Gln	Tyr	His	Asn	Asp
705					710					715					720
Phe	Ser	Leu	Arg	Arg	Tyr	Leu	Arg	Ala	Phe	Lys	Thr	Thr	Asp	Asp	Ala
			725						730					735	
Phe	Gln	Ala	Ile	Leu	Lys	Thr	Asn	Lys	Trp	Arg	Glu	Thr	Tyr	Gly	Val
			740					745					750		
Asp	Lys	Leu	Ser	Glu	Met	Asp	Arg	Ser	Gln	Leu	Asp	Lys	Lys	Ala	Arg
		755					760					765			
Leu	Leu	Arg	His	Arg	Asp	Cys	Ile	Gly	Arg	Pro	Val	Ile	Tyr	Ile	Pro
	770					775					780				
Ala	Lys	Asn	His	Ser	Ser	Glu	Arg	Asp	Ile	Asp	Glu	Leu	Thr	Arg	Phe
785					790					795					800
Ile	Val	Tyr	Asn	Leu	Glu	Glu	Ala	Cys	Lys	Lys	Cys	Phe	Glu	Glu	Val
			805						810					815	
Thr	Asp	Arg	Leu	Cys	Ile	Val	Phe	Asp	Leu	Ala	Glu	Phe	Ser	Thr	Ser
			820					825					830		
Cys	Met	Asp	Tyr	Gln	Leu	Val	Gln	Asn	Leu	Ile	Trp	Leu	Leu	Gly	Lys
		835					840					845			
His	Phe	Pro	Glu	Arg	Leu	Gly	Val	Cys	Leu	Ile	Ile	Asn	Ser	Pro	Gly
	850					855					860				
Leu	Phe	Ser	Thr	Ile	Trp	Pro	Ala	Ile	Arg	Val	Leu	Leu	Asp	Asp	Asn
865					870					875					880

Thr Ala Lys Lys Val Lys Phe Val Ala Asp Glu Ala Glu Leu Cys Gln
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Tyr Leu Ile Pro Asp Ile Leu Pro Thr Asp Met
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<211> 1875
<212> DNA
<213> Saccharomyces cerevisiae
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ttgagctgct	tgctctgtct	ggatgatgga	actttgagct	ctgatggagg	ttcttttgat	180	
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ccttttcaaa	cggaaaatct	gagttcttcg	tctgaaaatg	acgacgttga	gaatcatagt	360	
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gaaaattcca	agagaaacag	atcgatatta	gtcattatta	atccccacgg	tggttaaaggt	720	
actgctaaaa	atttattctt	gacaaaagca	aggccaatac	tagtggaagg	tggttgcaaa	780	
atagaaaattg	catacacaaa	atatgcccgt	cacggcatcg	atattgccaa	agatttgagat	840	
atcagcaaat	acgataccat	tgcattgtgc	tcgggtgatg	gtattccata	cgaagtaatt	900	
aatgggcttt	atagaagacc	cgacagagtg	gatgcgttca	ataaaactagc	cgtaactcag	960	
ctaccttgcg	gttcaggaaa	tgctatgagc	atttcatgtc	attggacaaa	taaccctatcg	1020	
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<210> 31
<211> 624
<212> PRT
<213> Saccharomyces cerevisiae
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Arg	Ser	Gly	Asp	Ser	Leu	Ser	Leu	Leu	Ser	Cys	Leu	Ser	Cys	Leu	Asp
		35					40					45			
Asp	Gly	Thr	Leu	Ser	Ser	Asp	Gly	Gly	Ser	Phe	Asp	Glu	Asp	Asp	Ser
	50					55					60				
Leu	Glu	Leu	Leu	Pro	Leu	Asn	Thr	Thr	Ile	Pro	Phe	Asn	Arg	Ile	Leu
65					70					75				80	
Asn	Ala	Lys	Tyr	Val	Asn	Val	Gly	Gln	Lys	Gly	Phe	Asn	Asn	Gly	Lys
				85					90					95	
Ile	Ser	Ser	Asn	Pro	Phe	Gln	Thr	Glu	Asn	Leu	Ser	Ser	Ser	Ser	Glu
			100					105					110		
Asn	Asp	Asp	Val	Glu	Asn	His	Ser	Leu	Ser	Asn	Asp	Lys	Ala	Pro	Val
		115					120					125			
Ser	Glu	Ser	Gln	Ser	Phe	Pro	Lys	Lys	Asp	Lys	Trp	Asp	Thr	Lys	Thr
	130					135					140				
Asn	Thr	Val	Lys	Val	Ser	Pro	Asp	Asp	Ser	Gln	Asp	Asn	Ser	Pro	Ser
145					150					155					160
Leu	Gly	Ile	Lys	Asp	Asn	Gln	Gln	Leu	Ile	Glu	Leu	Thr	Phe	Ala	Val
				165				170						175	
Pro	Lys	Gly	His	Asp	Val	Ile	Pro	Gln	Lys	Leu	Thr	Leu	Leu	Ile	Asp
			180					185					190		
His	Val	Ser	Arg	Lys	Ser	Arg	Ala	Asn	Thr	Gly	Glu	Glu	Asn	Ile	Ser
		195					200					205			
Ser	Gly	Thr	Val	Glu	Glu	Ile	Leu	Glu	Lys	Ser	Tyr	Glu	Asn	Ser	Lys
	210					215					220				
Arg	Asn	Arg	Ser	Ile	Leu	Val	Ile	Ile	Asn	Pro	His	Gly	Gly	Lys	Gly
225					230					235					240
Thr	Ala	Lys	Asn	Leu	Phe	Leu	Thr	Lys	Ala	Arg	Pro	Ile	Leu	Val	Glu
				245					250					255	
Ser	Gly	Cys	Lys	Ile	Glu	Ile	Ala	Tyr	Thr	Lys	Tyr	Ala	Arg	His	Ala
			260					265					270		
Ile	Asp	Ile	Ala	Lys	Asp	Leu	Asp	Ile	Ser	Lys	Tyr	Asp	Thr	Ile	Ala
	275						280					285			
Cys	Ala	Ser	Gly	Asp	Gly	Ile	Pro	Tyr	Glu	Val	Ile	Asn	Gly	Leu	Tyr
	290					295					300				
Arg	Arg	Pro	Asp	Arg	Val	Asp	Ala	Phe	Asn	Lys	Leu	Ala	Val	Thr	Gln
305					310					315					320
Leu	Pro	Cys	Gly	Ser	Gly	Asn	Ala	Met	Ser	Ile	Ser	Cys	His	Trp	Thr
				325					330					335	
Asn	Asn	Pro	Ser	Tyr	Ala	Ala	Leu	Cys	Leu	Val	Lys	Ser	Ile	Glu	Thr
			340					345					350		
Arg	Ile	Asp	Leu	Met	Cys	Cys	Ser	Gln	Pro	Ser	Tyr	Met	Asn	Glu	Trp
		355					360					365			
Pro	Arg	Leu	Ser	Phe	Leu	Ser	Gln	Thr	Tyr	Gly	Val	Ile	Ala	Glu	Ser
	370					375					380				
Asp	Ile	Asn	Thr	Glu	Phe	Ile	Arg	Trp	Met	Gly	Pro	Val	Arg	Phe	Asn
385					390					395					400
Leu	Gly	Val	Ala	Phe	Asn	Ile	Ile	Gln	Gly	Lys	Lys	Tyr	Pro	Cys	Glu
				405					410					415	
Val	Phe	Val	Lys	Tyr	Ala	Ala	Lys	Ser	Lys	Lys	Glu	Leu	Lys	Val	His
			420					425					430		
Phe	Leu	Glu	Asn	Lys	Asp	Lys	Asn	Lys	Gly	Cys	Leu	Thr	Phe	Glu	Pro
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Asn Pro Ser Pro Asn Ser Ser Pro Asp Leu Leu Ser Lys Asn Asn Ile
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Asn Asn Ser Thr Lys Asp Glu Leu Ser Pro Asn Phe Leu Asn Glu Asp
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Asn Phe Lys Leu Lys Tyr Pro Met Thr Glu Pro Val Pro Arg Asp Trp
                      485                      490                      495
Glu Lys Met Asp Ser Glu Leu Thr Asp Asn Leu Thr Ile Phe Tyr Thr
                      500                      505                      510
Gly Lys Met Pro Tyr Ile Ala Lys Asp Thr Lys Phe Phe Pro Ala Ala
  515                      520                      525
Leu Pro Ala Asp Gly Thr Ile Asp Leu Val Ile Thr Asp Ala Arg Ile
  530                      535                      540
Pro Val Thr Arg Met Thr Pro Ile Leu Leu Ser Leu Asp Lys Gly Ser
545                      550                      555                      560
His Val Leu Glu Pro Glu Val Ile His Ser Lys Ile Leu Ala Tyr Lys
                      565                      570                      575
Ile Ile Pro Lys Val Glu Ser Gly Leu Phe Ser Val Asp Gly Glu Lys
                      580                      585                      590
Phe Pro Leu Glu Pro Leu Gln Val Glu Ile Met Pro Met Leu Cys Lys
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Thr Leu Leu Arg Asn Gly Arg Tyr Ile Asp Thr Glu Phe Glu Ser Met
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<210> 32

<211> 2064

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 32

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gtaaagtatg ctgccaaatc aaaaaacgag ttaaaaaatc attacctgga acacaaaaat 1440

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<210> 33

<211> 687

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 33

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Ile Lys Ala Lys Pro Ser Ser Pro Tyr Thr Tyr Ala Asn Arg Met Ala
      35          40          45
Asp Lys Arg Ser Arg Ser Ser Ile Asp Asn Ile Ser Arg Thr Ser Phe
 50          55          60
Gln Ser Asn Ile Ser Arg Thr Ser Phe Gln Ser Asn Ser Asp Asn Asn
 65          70          75          80
Ser Ile Phe Glu Thr Ala Ser Leu Ile Ser Cys Val Thr Cys Leu Ser
      85          90          95
Asp Thr Asp Thr Ile Asp Arg Ser Glu Thr Ser Thr Thr Asp Thr Ser
      100          105          110
Lys Asp Asp Leu Ser Ala Asn Pro Lys Leu His Tyr Pro Ser Val Asn
      115          120          125
Gly Gln Leu Pro Ala Asn Thr Val Ile Pro Tyr Gly Arg Ile Leu Asp
      130          135          140
Ala Arg Tyr Ile Glu Lys Glu Pro Leu His Tyr Tyr Asp Ala Asn Ser
      145          150          155          160
Ser Pro Ser Ser Pro Leu Ser Ser Ser Met Ser Asn Ile Ser Glu Lys
      165          170          175
Cys Asp Leu Asp Glu Leu Glu Ser Ser Gln Lys Lys Glu Arg Lys Gly
      180          185          190
Asn Ser Leu Ser Arg Gly Ser Asn Ser Ser Ser Ser Leu Leu Thr Ser
      195          200          205
Arg Ser Pro Phe Thr Lys Leu Val Glu Val Ile Phe Ala Arg Pro Arg
      210          215          220
Arg His Asp Val Val Pro Lys Arg Val Ser Leu Tyr Ile Asp Tyr Lys
      225          230          235          240
Pro His Ser Ser Ser His Leu Lys Glu Glu Asp Asp Leu Val Glu Glu
      245          250          255
Ile Leu Lys Arg Ser Tyr Lys Asn Thr Arg Arg Asn Lys Ser Ile Phe
      260          265          270
Val Ile Ile Asn Pro Phe Gly Gly Lys Gly Lys Ala Lys Lys Leu Phe
      275          280          285

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Met	Asp	Ile	Asp	Lys	Tyr	Asp	Thr	Ile	Ala	Cys	Ala	Ser	Gly	Asp	Gly	325	330	335
Ile	Pro	His	Glu	Val	Ile	Asn	Gly	Leu	Tyr	Gln	Arg	Pro	Asp	His	Val	340	345	350
Lys	Ala	Phe	Asn	Asn	Ile	Ala	Ile	Thr	Glu	Ile	Pro	Cys	Gly	Ser	Gly	355	360	365
Asn	Ala	Met	Ser	Val	Ser	Cys	His	Trp	Thr	Asn	Asn	Pro	Ser	Tyr	Ser	370	375	380
Thr	Leu	Cys	Leu	Ile	Lys	Ser	Ile	Glu	Thr	Arg	Ile	Asp	Leu	Met	Cys	385	390	395
Cys	Ser	Gln	Pro	Ser	Tyr	Ala	Arg	Glu	His	Pro	Lys	Leu	Ser	Phe	Leu	405	410	415
Ser	Gln	Thr	Tyr	Gly	Leu	Ile	Ala	Glu	Thr	Asp	Ile	Asn	Thr	Glu	Phe	420	425	430
Ile	Arg	Trp	Met	Gly	Pro	Ala	Arg	Phe	Glu	Leu	Gly	Val	Ala	Phe	Asn	435	440	445
Ile	Ile	Gln	Lys	Lys	Lys	Tyr	Pro	Cys	Glu	Ile	Tyr	Val	Lys	Tyr	Ala	450	455	460
Ala	Lys	Ser	Lys	Asn	Glu	Leu	Lys	Asn	His	Tyr	Leu	Glu	His	Lys	Asn	465	470	475
Lys	Gly	Ser	Leu	Glu	Phe	Gln	His	Ile	Thr	Met	Asn	Lys	Asp	Asn	Glu	485	490	495
Asp	Cys	Asp	Asn	Tyr	Asn	Tyr	Glu	Asn	Glu	Tyr	Glu	Thr	Glu	Asn	Glu	500	505	510
Asp	Glu	Asp	Glu	Asp	Ala	Asp	Ala	Asp	Asp	Glu	Asp	Ser	His	Leu	Ile	515	520	525
Ser	Arg	Asp	Leu	Ala	Asp	Ser	Ser	Ala	Asp	Gln	Ile	Lys	Glu	Glu	Asp	530	535	540
Phe	Lys	Ile	Lys	Tyr	Pro	Leu	Asp	Glu	Gly	Ile	Pro	Ser	Asp	Trp	Glu	545	550	555
Arg	Leu	Asp	Pro	Asn	Ile	Ser	Asn	Asn	Leu	Gly	Ile	Phe	Tyr	Thr	Gly	565	570	575
Lys	Met	Pro	Tyr	Val	Ala	Ala	Asp	Thr	Lys	Phe	Phe	Pro	Ala	Ala	Leu	580	585	590
Pro	Ser	Asp	Gly	Thr	Met	Asp	Met	Val	Ile	Thr	Asp	Ala	Arg	Thr	Ser	595	600	605
Leu	Thr	Arg	Met	Ala	Pro	Ile	Leu	Leu	Gly	Leu	Asp	Lys	Gly	Ser	His	610	615	620
Val	Leu	Gln	Pro	Glu	Val	Leu	His	Ser	Lys	Ile	Leu	Ala	Tyr	Lys	Ile	625	630	635
Ile	Pro	Lys	Leu	Gly	Asn	Gly	Leu	Phe	Ser	Val	Asp	Gly	Glu	Lys	Phe	645	650	655
Pro	Leu	Glu	Pro	Leu	Gln	Val	Glu	Ile	Met	Pro	Arg	Leu	Cys	Lys	Thr	660	665	670
Leu	Leu	Arg	Asn	Gly	Arg	Tyr	Val	Asp	Thr	Asp	Phe	Asp	Ser	Met		675	680	685

<210> 34

<211> 1230

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 34

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cgaactcgaa tgtccaaatt tcggtttaat attagagaga agctgttagt gtttaccac 180
aatcaatcat tcacattaag ccgctggcaa aagaagtacc gttctgcgtt taatgatctc 240
tactttactt atacttcctt aatgggatcg cataccttct atgttctgtg tttacctatg 300
cccgtgtggt ttggatattt tgaacaaca aaagatatgg tttatatctt gggatattct 360
atctacttga gtggtttttt taaagattac tgggtgcttg ccaggcctag agcacctcca 420
ttacatcgaa ttacgttaag tgaatataca acgaaggaat atggtgctcc aagctcccat 480
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tcttctgtca tgggtccact attgttgtca tgtgtgggtt tattttatta tatgactttg 600
gttttcggtg gaatatactg tgggatgcat ggcataattag atttagtaag cgggtgggctc 660
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attgaggagc attggtggtt tcctttgttt agtgtgggat ggggtcttct tcttttgttt 780
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gttgtgtcag gtattgaatg ctgtgattgg ttgggcaaag tgtttggagt caccctggtg 900
tacaatttgg aacctaaactg tggctggcgg ttaaccttag ccaggctgct ggtgggccta 960
ccgtgcgttg ttatctggaa gtacgtgatc agcaaaccga tgatctacac gttattgatc 1020
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caciaaagaag gtgcaagcaa gtacgaatgt ccattatata ttggagagcc caagattgac 1140
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<210> 35

<211> 409

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 35

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Met Val Asp Gly Leu Asn Thr Ser Asn Ile Arg Lys Arg Ala Arg Thr
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Leu Ser Asn Pro Asn Asp Phe Gln Glu Pro Asn Tyr Leu Leu Asp Pro
          20          25          30
Gly Asn His Pro Ser Asp His Phe Arg Thr Arg Met Ser Lys Phe Arg
          35          40          45
Phe Asn Ile Arg Glu Lys Leu Leu Val Phe Thr Asn Asn Gln Ser Phe
          50          55          60
Thr Leu Ser Arg Trp Gln Lys Lys Tyr Arg Ser Ala Phe Asn Asp Leu
65          70          75          80
Tyr Phe Thr Tyr Thr Ser Leu Met Gly Ser His Thr Phe Tyr Val Leu
          85          90          95
Cys Leu Pro Met Pro Val Trp Phe Gly Tyr Phe Glu Thr Thr Lys Asp
          100          105          110
Met Val Tyr Ile Leu Gly Tyr Ser Ile Tyr Leu Ser Gly Phe Phe Lys
          115          120          125
Asp Tyr Trp Cys Leu Pro Arg Pro Arg Ala Pro Pro Leu His Arg Ile
          130          135          140
Thr Leu Ser Glu Tyr Thr Thr Lys Glu Tyr Gly Ala Pro Ser Ser His
145          150          155          160
Thr Ala Asn Ala Thr Gly Val Ser Leu Leu Phe Leu Tyr Asn Ile Trp
          165          170          175

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Arg Met Gln Glu Ser Ser Val Met Val Gln Leu Leu Leu Ser Cys Val
 180 185 190
 Val Leu Phe Tyr Tyr Met Thr Leu Val Phe Gly Arg Ile Tyr Cys Gly
 195 200 205
 Met His Gly Ile Leu Asp Leu Val Ser Gly Gly Leu Ile Gly Ile Val
 210 215 220
 Cys Phe Ile Val Arg Met Tyr Phe Lys Tyr Arg Phe Pro Gly Leu Arg
 225 230 235 240
 Ile Glu Glu His Trp Trp Phe Pro Leu Phe Ser Val Gly Trp Gly Leu
 245 250 255
 Leu Leu Leu Phe Lys His Val Lys Pro Val Asp Glu Cys Pro Cys Phe
 260 265 270
 Gln Asp Ser Val Ala Phe Met Gly Val Val Ser Gly Ile Glu Cys Cys
 275 280 285
 Asp Trp Leu Gly Lys Val Phe Gly Val Thr Leu Val Tyr Asn Leu Glu
 290 295 300
 Pro Asn Cys Gly Trp Arg Leu Thr Leu Ala Arg Leu Leu Val Gly Leu
 305 310 315 320
 Pro Cys Val Val Ile Trp Lys Tyr Val Ile Ser Lys Pro Met Ile Tyr
 325 330 335
 Thr Leu Leu Ile Lys Val Phe His Leu Lys Asp Asp Arg Asn Val Ala
 340 345 350
 Ala Arg Lys Arg Leu Glu Ala Thr His Lys Glu Gly Ala Ser Lys Tyr
 355 360 365
 Glu Cys Pro Leu Tyr Ile Gly Glu Pro Lys Ile Asp Ile Leu Gly Arg
 370 375 380
 Phe Ile Ile Tyr Ala Gly Val Pro Phe Thr Val Val Met Cys Ser Pro
 385 390 395 400
 Val Leu Phe Ser Leu Asn Ile Ala
 405

<210> 36

<211> 1215

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 36

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 tttagagacc agatgtcgtg gctaagggtt caaacaaggc agtatctaac tagattcaca 180
 gacaaccaat cagatttcgt acattcttta caaaaaaagc acagaacgcc ttttagagac 240
 gtttatttca aatacacttc gcttatgggt tcccacatgt tttatgttat cgtgcttccc 300
 atgcctgtgt ggcttgata ccgcgattta acacgggaca tgatctacgt tcttggttat 360
 tcaatttatt tgagtggcta cttaaaggat tattggtgcc taccaaggcc aaaatcaccg 420
 ccagttgaca gaatcacact aagtgaatac actacgaaag aatatggtgc acccagttca 480
 cattctgcta acgctactgc ggtaagtcta ttattctttt ggagaatatg tttatctgac 540
 aactggtat ggccaacaaa gcttctttta ctgagctctg tgatatttta ctacttaacc 600
 ctggtttttg gtagagttaa ctgcggtatg catggtatgc tggatttatt tagcggcgcc 660
 gcagttggag ctatctgttt tttataaga atctgggtgg tgcattgctt acgaaatttc 720
 cagattggtg aacatctctg gtttcccctt ttgagttag catggggctt gtttattctg 780
 ttaaccacg tcaggcccat tgatgaatgt ccttggttcg aagatagcgt agcgttcatt 840
 ggcgtagtca gtgggctgga ttgcagcgac tggttaaccg aaagatacgg atggaacctt 900
 gtatgtagta ggtacgcata atgtggttct aagggtgtct tgaggcctct ggtaggtgtc 960

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gcttctgtga ttgtttggaa agacgtcatt agcaagacag ctgtctacac gctgttaatt 1020
aaactactca gatttcacga tgatagaagc gaaaagggttc atttccataa cgagacaagt 1080
gaagaagaag agtgttttatt gtacagcggg gtttccaaag tggaaatcgt cggaagggttt 1140
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acaaacttaa ggtag 1215

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<210> 37

<211> 404

<212> PRT

<213> *Sacchromyces cerevisiae*

<400> 37

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Ile Lys Val Gln Met Ala Pro Ser Gly Gly Lys His Leu Leu Ala Asp
 20          25          30
Pro Gly Asn His Pro Ala Glu His Phe Glu Ser Gln Met Ser Trp Leu
 35          40          45
Arg Phe Gln Thr Arg Gln Tyr Leu Thr Arg Phe Thr Asp Asn Gln Ser
 50          55          60
Asp Phe Val His Ser Leu Gln Lys Lys His Arg Thr Pro Phe Arg Asp
 65          70          75          80
Val Tyr Phe Lys Tyr Thr Ser Leu Met Gly Ser His Met Phe Tyr Val
 85          90          95
Ile Val Leu Pro Met Pro Val Trp Leu Gly Tyr Arg Asp Leu Thr Arg
100          105          110
Asp Met Ile Tyr Val Leu Gly Tyr Ser Ile Tyr Leu Ser Gly Tyr Leu
115          120          125
Lys Asp Tyr Trp Cys Leu Pro Arg Pro Lys Ser Pro Pro Val Asp Arg
130          135          140
Ile Thr Leu Ser Glu Tyr Thr Thr Lys Glu Tyr Gly Ala Pro Ser Ser
145          150          155          160
His Ser Ala Asn Ala Thr Ala Val Ser Leu Leu Phe Phe Trp Arg Ile
165          170          175
Cys Leu Ser Asp Thr Leu Val Trp Pro Thr Lys Leu Leu Leu Leu Ser
180          185          190
Leu Val Ile Phe Tyr Tyr Leu Thr Leu Val Phe Gly Arg Val Tyr Cys
195          200          205
Gly Met His Gly Met Leu Asp Leu Phe Ser Gly Ala Ala Val Gly Ala
210          215          220
Ile Cys Phe Phe Ile Arg Ile Trp Val Val His Ala Leu Arg Asn Phe
225          230          235          240
Gln Ile Gly Glu His Leu Trp Phe Pro Leu Leu Ser Val Ala Trp Gly
245          250          255
Leu Phe Ile Leu Phe Asn His Val Arg Pro Ile Asp Glu Cys Pro Cys
260          265          270
Phe Glu Asp Ser Val Ala Phe Ile Gly Val Val Ser Gly Leu Asp Cys
275          280          285
Ser Asp Trp Leu Thr Glu Arg Tyr Gly Trp Asn Leu Val Cys Ser Arg
290          295          300
Tyr Ala Ser Cys Gly Ser Lys Val Phe Leu Arg Pro Leu Val Gly Val
305          310          315          320
Ala Ser Val Ile Val Trp Lys Asp Val Ile Ser Lys Thr Ala Val Tyr
325          330          335

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Thr Leu Leu Ile Lys Leu Leu Arg Phe His Asp Asp Arg Ser Glu Lys
 340 345 350
 Val His Phe His Asn Glu Thr Ser Glu Glu Glu Glu Cys Leu Leu Tyr
 355 360 365
 Ser Gly Val Ser Lys Val Glu Ile Val Gly Arg Phe Leu Ile Tyr Ala
 370 375 380
 Gly Ile Pro Thr Thr Val Phe Leu Leu Cys Pro Val Phe Phe Thr Trp
 385 390 395 400
 Thr Asn Leu Arg

<210> 38

<211> 1050

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 38

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tccttgctgc cggaatgag tgatggtgtg ctggccttgg ttgcgccggt tgttgcttac 180
tgggcggttg ctggtatatt ccatgtaata gacactttcc atctggctga gaagtacaga 240
attcatccga gcgaagaggt tgccaagagg aacaaggcgt cgagaatgca tgttttcctt 300
gaagtgattc tacaacatat catacagacc attggtggcc ttatctttat gcacttcgag 360
ccgatctaca tgactggggt tgaagaaaat gccatgtgga agcttcgtgc agaccttcct 420
cggattattc cagatgccgc tatttattac ggctatatgt acggaatgac cgctttgaag 480
atctttgcag gctttttatt cggtgataca tggcaatact ttttgcatag attgatgcat 540
atgaataaga ccttatacaa atgggtccac tctgttcac atgaactata cgtgccatat 600
gcttacgggtg ctcttttcaa caatcctggt gagggcttct tgtagatac tttgggaacc 660
ggtattgcca tgacgttaac tcatttgact cacagagagc aaatcattct ttttaccttt 720
gccaccatga agactgtcga tgaccactgt ggggtatgct tgccacttga cccattccaa 780
tggtttttcc ctaataacgc tgtctatcac gatatccacc accagcaatt tggtatcaag 840
acgaactttg ctcaaccatt tttcactttc tgggacaatt tgttccaaac taactttaaa 900
gggtttgaag aatatcaaaa gaagcaaaga cgtgtcacca tcgacaagta caaagagttt 960
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gctgaaaatg aagtaaagaa agagaaataa 1050

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<210> 39

<211> 349

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 39

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 Phe Gly Leu Lys Thr Ser Phe Gly Phe Met His Tyr Ala Lys Ala Pro
 20 25 30
 Ala Ile Asn Leu Arg Pro Lys Glu Ser Leu Leu Pro Glu Met Ser Asp
 35 40 45
 Gly Val Leu Ala Leu Val Ala Pro Val Val Ala Tyr Trp Ala Leu Ser
 50 55 60
 Gly Ile Phe His Val Ile Asp Thr Phe His Leu Ala Glu Lys Tyr Arg
 65 70 75 80
 Ile His Pro Ser Glu Glu Val Ala Lys Arg Asn Lys Ala Ser Arg Met

				85					90					95		
His	Val	Phe	Leu	Glu	Val	Ile	Leu	Gln	His	Ile	Ile	Gln	Thr	Ile	Val	
			100					105					110			
Gly	Leu	Ile	Phe	Met	His	Phe	Glu	Pro	Ile	Tyr	Met	Thr	Gly	Phe	Glu	
		115					120					125				
Glu	Asn	Ala	Met	Trp	Lys	Leu	Arg	Ala	Asp	Leu	Pro	Arg	Ile	Ile	Pro	
	130					135					140					
Asp	Ala	Ala	Ile	Tyr	Tyr	Gly	Tyr	Met	Tyr	Gly	Met	Ser	Ala	Leu	Lys	
145				150						155					160	
Ile	Phe	Ala	Gly	Phe	Leu	Phe	Val	Asp	Thr	Trp	Gln	Tyr	Phe	Leu	His	
			165					170						175		
Arg	Leu	Met	His	Met	Asn	Lys	Thr	Leu	Tyr	Lys	Trp	Phe	His	Ser	Val	
			180					185					190			
His	His	Glu	Leu	Tyr	Val	Pro	Tyr	Ala	Tyr	Gly	Ala	Leu	Phe	Asn	Asn	
		195				200						205				
Pro	Val	Glu	Gly	Phe	Leu	Leu	Asp	Thr	Leu	Gly	Thr	Gly	Ile	Ala	Met	
	210					215					220					
Thr	Leu	Thr	His	Leu	Thr	His	Arg	Glu	Gln	Ile	Ile	Leu	Phe	Thr	Phe	
225				230						235					240	
Ala	Thr	Met	Lys	Thr	Val	Asp	Asp	His	Cys	Gly	Tyr	Ala	Leu	Pro	Leu	
			245					250						255		
Asp	Pro	Phe	Gln	Trp	Leu	Phe	Pro	Asn	Asn	Ala	Val	Tyr	His	Asp	Ile	
			260					265					270			
His	His	Gln	Gln	Phe	Gly	Ile	Lys	Thr	Asn	Phe	Ala	Gln	Pro	Phe	Phe	
		275					280					285				
Thr	Phe	Trp	Asp	Asn	Leu	Phe	Gln	Thr	Asn	Phe	Lys	Gly	Phe	Glu	Glu	
	290					295					300					
Tyr	Gln	Lys	Lys	Gln	Arg	Arg	Val	Thr	Ile	Asp	Lys	Tyr	Lys	Glu	Phe	
305				310						315					320	
Leu	Gln	Glu	Arg	Glu	Leu	Glu	Lys	Lys	Glu	Lys	Leu	Lys	Asn	Phe	Lys	
				325				330						335		
Ala	Met	Asn	Ala	Ala	Glu	Asn	Glu	Val	Lys	Lys	Glu	Lys				
			340					345								

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<210> 40
<211> 32
<212> DNA
<213> Artificial Sequence
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<220>
<223> PCR primer

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<400> 40
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32

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<210> 41
<211> 30
<212> DNA
<213> Artificial Sequence
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<220>
<223> PCR primer

<400> 41
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30